

Fig. 1

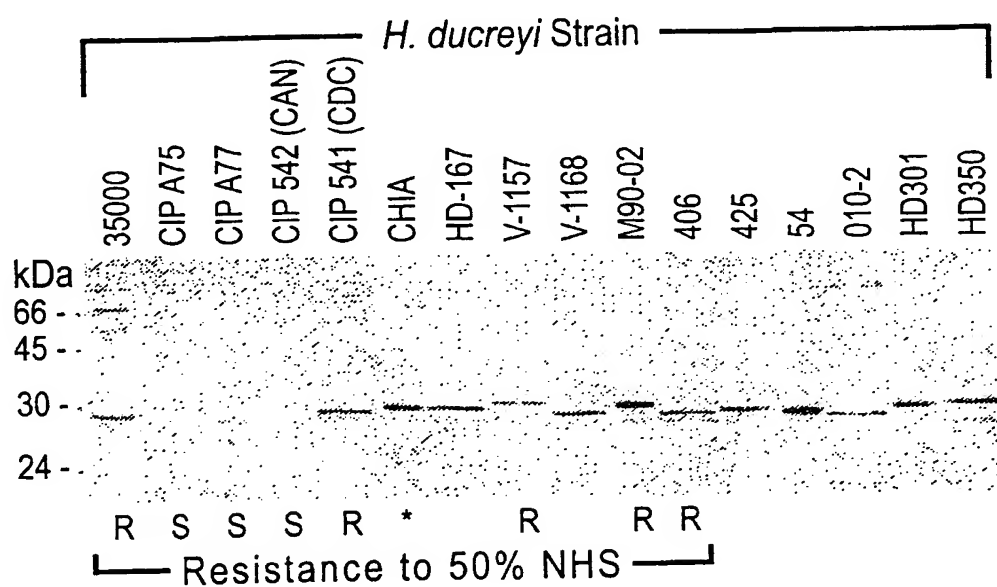
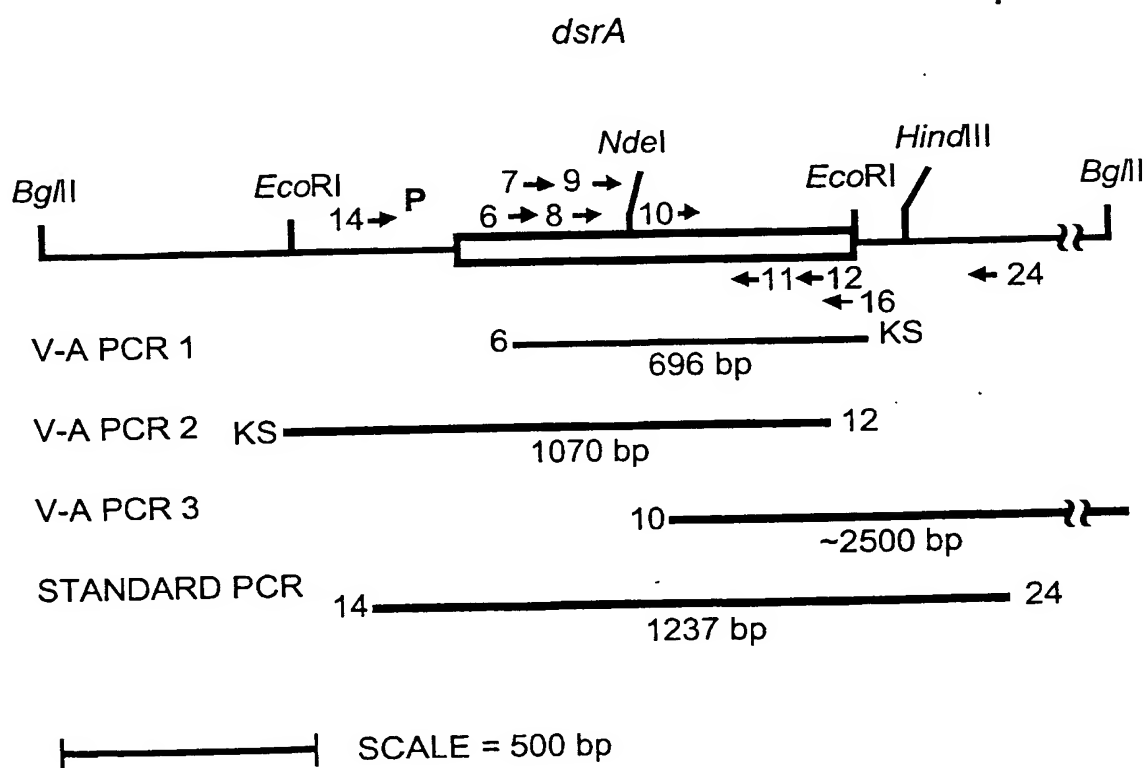


Fig. 2



## Fig. 3

1 ATAAATACGTCATTGACATTTTTTTTAAATGTAAGGTAGAATAAGAAAGTAAATCTATATTTACAATCAAGATTGACAATTTATTTACTTAATGAGGTGATT  
RBS  
-35 -10

101 ATGAAAATTAATGTTTAGTTGCCGTAGTGGGATTAGCTTGTCTACTATTAACAACAATGGCTCAGCAGCGCCCAAGTTTGGCTGGAGTATCTTCTTTGT  
1 M K I K C L V A V V G L A C S T I T T M A Q P P K F A G V S S L Y

201 ATAGCTATGAGTATGACTATGGTAAGGGTAAATGGACTTGGTCTAATGAAGGCGGTTTCGATATTAAGTGCCAGGGGATTAATAATGAAGCCAAAAGAATG  
35 S Y E Y D Y G K G K W T W S N E G G F D I K V P G I K M K P K E W

301 GATTCTAAACAGGCTACTTATCTTGAATTACAGCATTTATATGCCCTTATACCTCTGTCTCGTGACATATGCTCCTGGCGTTTCTCCTAGCCCTATACTG  
68 I S K Q A T Y L E L Q H Y M P Y T P V L V T Y A P G V S P S P I L

401 TTATATCCGATGTCTGATCCTGATCAACTTGGAAATAATCGGCAGCAGCTGAAATTTGAATTTGTATAGTTATTTTAAAGATTTAAGACACGATTTTAAAT  
101 L Y P M S D P D Q L G I N R Q Q L K L N L Y S Y F N D L R H D F K L

501 TAAAGTCTTGATGCACGTATTTCCAAAAATAAAACAAAATATTGATACATAAGTAAATATTACTAGAACTGGGTACTTATTTAGATGATCTTATCG  
135 K V L D A R I S K N K Q N I D T I S K Y L L E L G T Y L D D S Y R

601 TATGATGGAACAAAATACACATAATATCAATAAAGTTGTCTTAAAGAAATGCAAACTGGTTTAGCCCAACCAATCAGCATTCCTATGTTAGTGCAACCAAT  
168 M M E Q N T H N I N K L S K E L Q T G L A N Q S A L S M L V Q P N

701 GGTGTAGGCAAAAACGAGCGTTTCTGTGCGGTAGGAGGTTATAGAGATAAACTGCATTAGCCATTGGTGTGCGGTACGCAATTTACTGATCGCTTTACCG  
201 G V G K T S V S A A V G G Y R D K T A L A I G V G S R I T D R F T A

801 CTAAAGCGGTGTAGCGTTCAATACCTACAATGGCGGCATGTCTTATGGTGTCTCTGTGTGTTATGAATTCATCAATTCAGTTTAAATCACTAATCGTTT  
235 K A G V A F N T Y N G G M S Y G A S V G Y E F \*

901 TGGTTATAATAAAAGGCTAAATGTTTCTCCTCACAATTAGCCCTTCTTATTTATGCTTTTGTGTTATAGCTTTTGTCTGTTATAAAACCGTTTCTTTTAGCCACTT  
----->  
<-----

1	Dsra	1	QOPPKF	6
1	UsPa2	90	QVVEQFPNFFNENHDELDAYHNMILGDTAIVSNSQDNSTQLKFYSNDESDVPDLSLLFSKLLHEQQLNGFKAGDTIIPLDKDGKPVYT	
1	YaDa	56	-----DDYDGIPNLTAQISPNADPALGLEYPVRPPVPGA-----GGLNASAKGIHSIAIGATAEA-----	
7	Dsra	29	-----ACVSSMYSY-----EY-----DYG-----KGKWT-----WSNE	
46	UsPa2	180	KDTRTKDGKVETVYSTTKIATQDDVEQSAYSRGTQGDIDDLIDNREVNEXLKATHDYNERQTEAIDALNKASSANTDRIDTA EERIDK	
57	YaDa	117	-----AKGAAVAGAGSIATGVNS-----VAIGPE-----SKALGD-----SAVTYGAASTAQKDGVAI GARASTSDTGVA-----	
30	Dsra	55	-----VPGIKMKKEKEMISKQATVIF-----	
181	UsPa2	270	NEYDIKRALESNVEEGLEESGHLIDQKADITKDIKALESNVEEGLESDGLIDQKADLTQDIKALESNVEEGLLDLSGRLLDQKADIAK	
118	YaDa	195	-----SVAIGHSSHVAAHGYSTAI GDRSKTDRENSVSI GHESLNRLTHLAAGTKD-----TDAVNVAQLKKEIEK	
56	Dsra	121	-----LOHMPYTPVLVTYAPGVSPSPITPPNMSDBDQELGNROOLKI-----NEYSYFNDL-RHDFKLKVJD-----ARIS	
271	UsPa2	360	NQADIAQNQTDITQDLAAYNELQDAYAKQOQTEAIDALNKASSNTQNI AKNQADTANNINNI YELAQOQDQHSPIKTLAKASAA NTDRIA	
196	YaDa	265	TQENTNKRSAEULLANAN-----AYADNKSSSV-----LGIANNYTDKSAETJENARKEAFA-----QSKDVLMNAKAHNSV AR-----	
122	Dsra	144	-----KNKQNTDTI-----SKY-----LEELGT-----Y-----LDDDS	
361	UsPa2	450	KNKADADA SFETLTKNQNTLIEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSTIDLGTKVDGDFGRVTALDTK	
266	YaDa	335	-----TTLETAEEHANSV-----ARTTLETAEE-----HANKKSAEALASANVYADSKSSHT L-KTANSYTDVTVS-----NSTKKA IRES	
145	Dsra	229	-----YRMMEQNTHN-----JANKLSKELOGLANOSALSMIVOPNGVGGKTSVSAAVGGYRDKTALATGVGSRITDRTAKAGVAINTYANGGM-SYG	
451	UsPa2	540	YNAIDTKYNAFDGRITALDSKVENGMAQAATSGLEOPYSVGKFNATAALGGYSGSKSAVAIGAGYRVNPNLAFKAGAAINTSGNKKGSYN	
336	YaDa	423	NQYTDHKFRQDLNRIDKLDTRVDKGLASSAALNLSLEOPYGVGKYNETTAGVGGYRVSQALATGSGYRVNENVALKAGVAYAGSSDWM--YN	
230	Dsra		-----ASVGIEF-----	
541	UsPa2		-----IGVNIYEF-----	
424	YaDa		-----ASENIEW-----	

Fig. 5

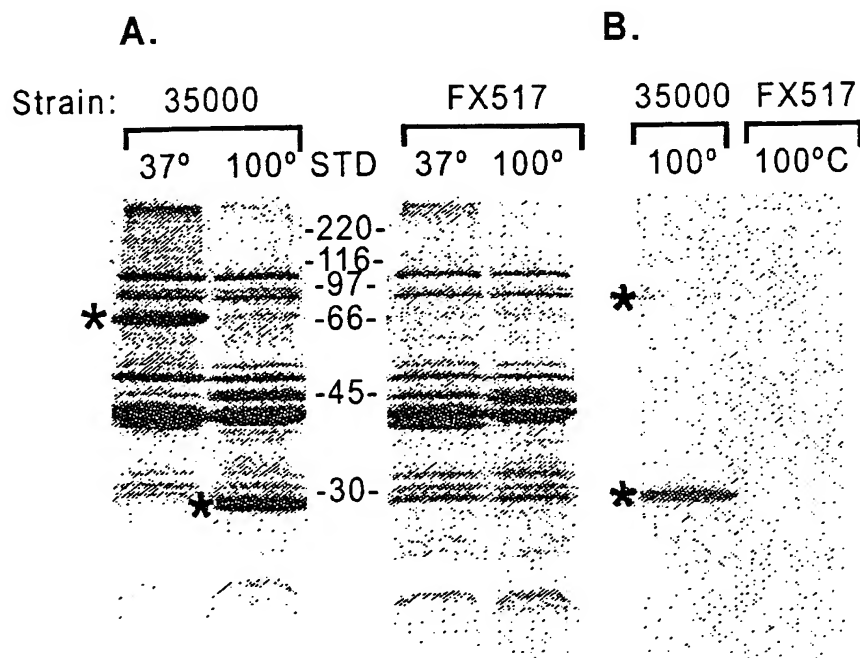


Fig. 6

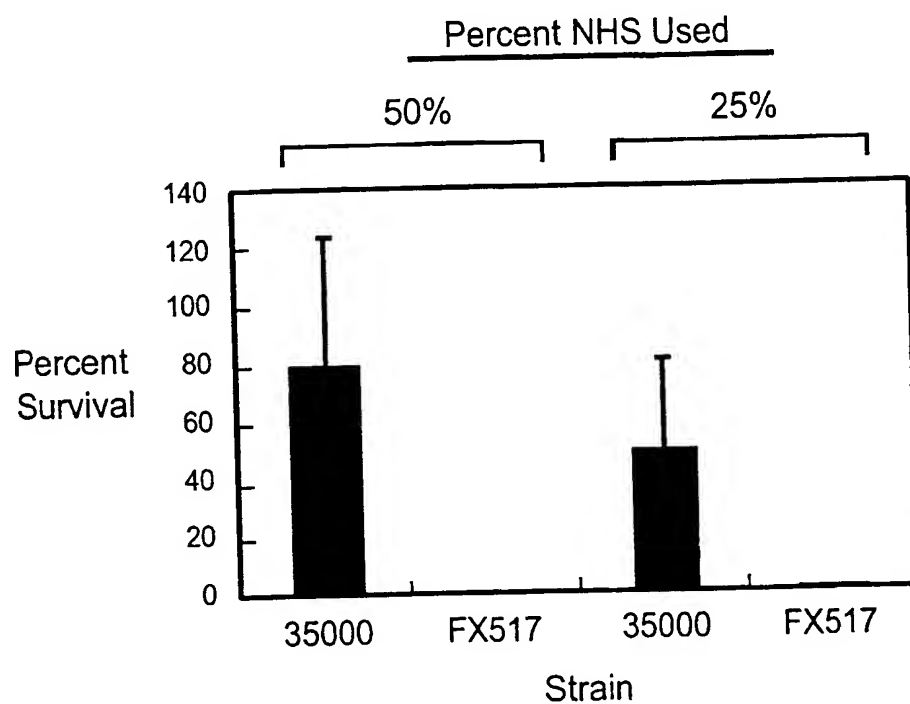


Fig. 7

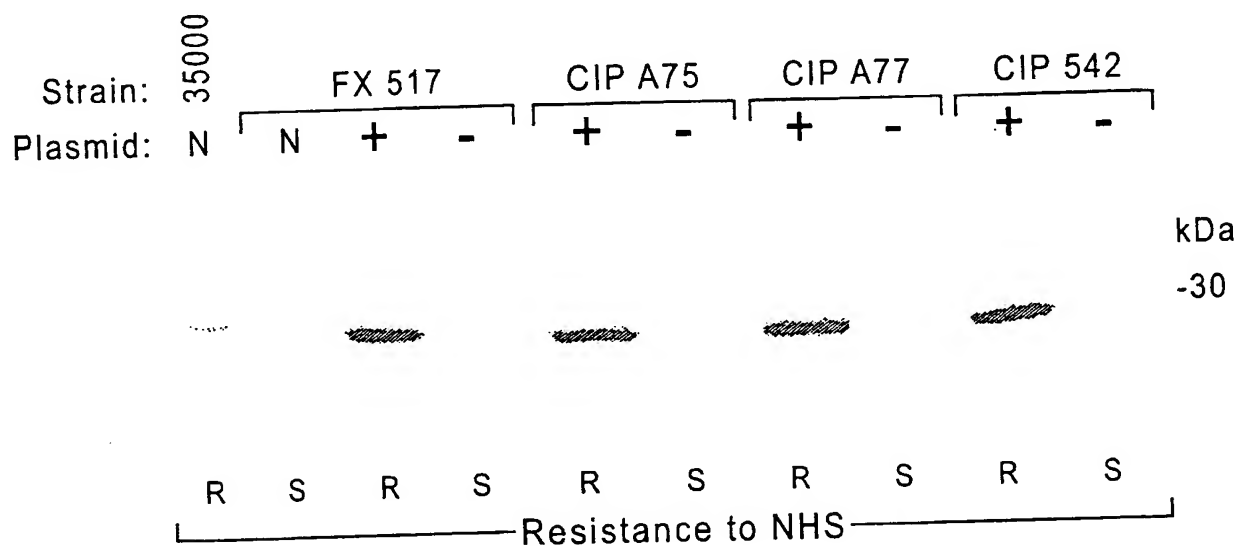
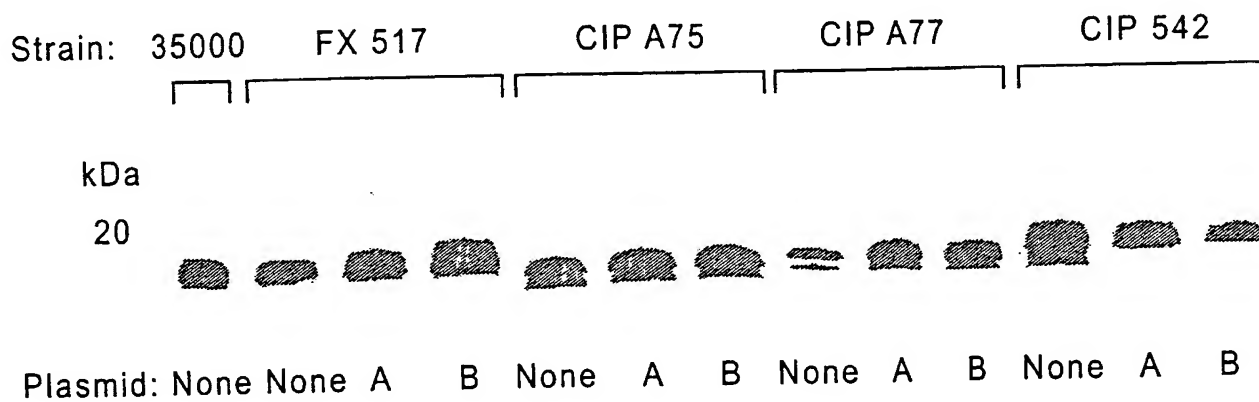


Fig. 8





9  
b  
i

\* = Variable Region 1

# = Variable Region 2 (Repeat Region)

Fig. 10

	<u>-35</u>	<u>-10</u>
35000	TTGACATTTTTTTTAATGTAAGGTAGAAT	
CIP A75	TTGACATTTTTTTTA-----AGGTAGAAT	
CIP A77	TTGACATTTTTTTTA-----AGGTAGAAT	
CIP 542 (CAN)	TTGACATTTTTTTTAATGTAAGGTAGAAT	
CIP 542 (CDC)	TTGACATTTTTTTTAATGTAAGGTAGAAT	
CHIA	TTGACATTTCTTTTAATGTAAGGTAAAAT	
V-1157	TTGACATTTTTTTTAATGTAAGGTAGAAT	
M90-02	TTGACATTTTTTTTAATGTAAGGTAGAAT	
406	TTGACATTTTTTTTAATGTAAGGTAGAAT	
	10	20
		30

Fig. 11

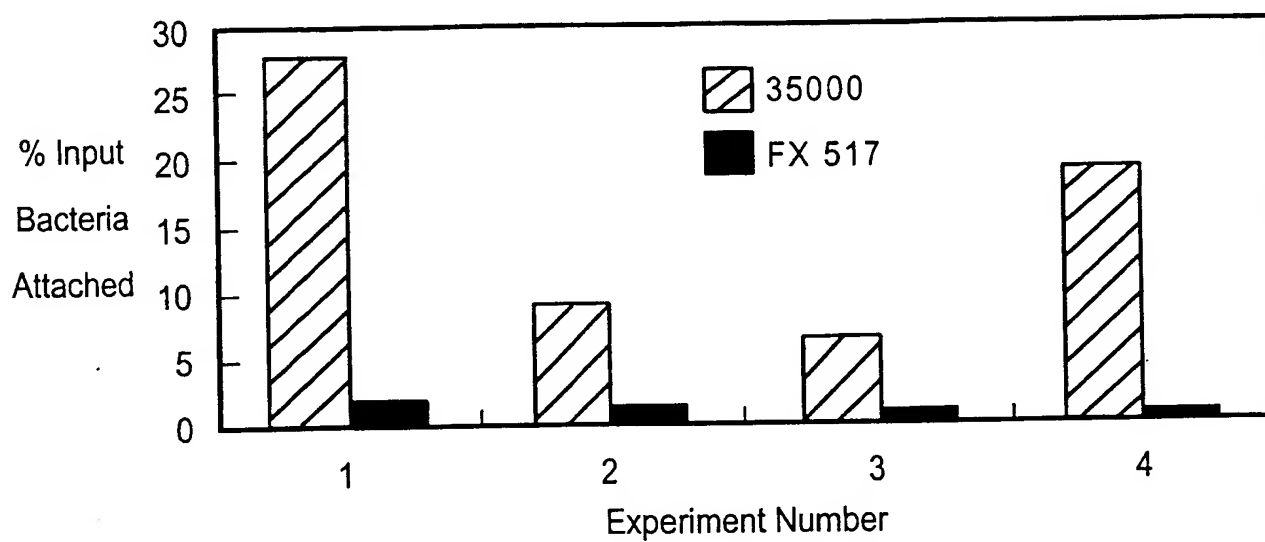
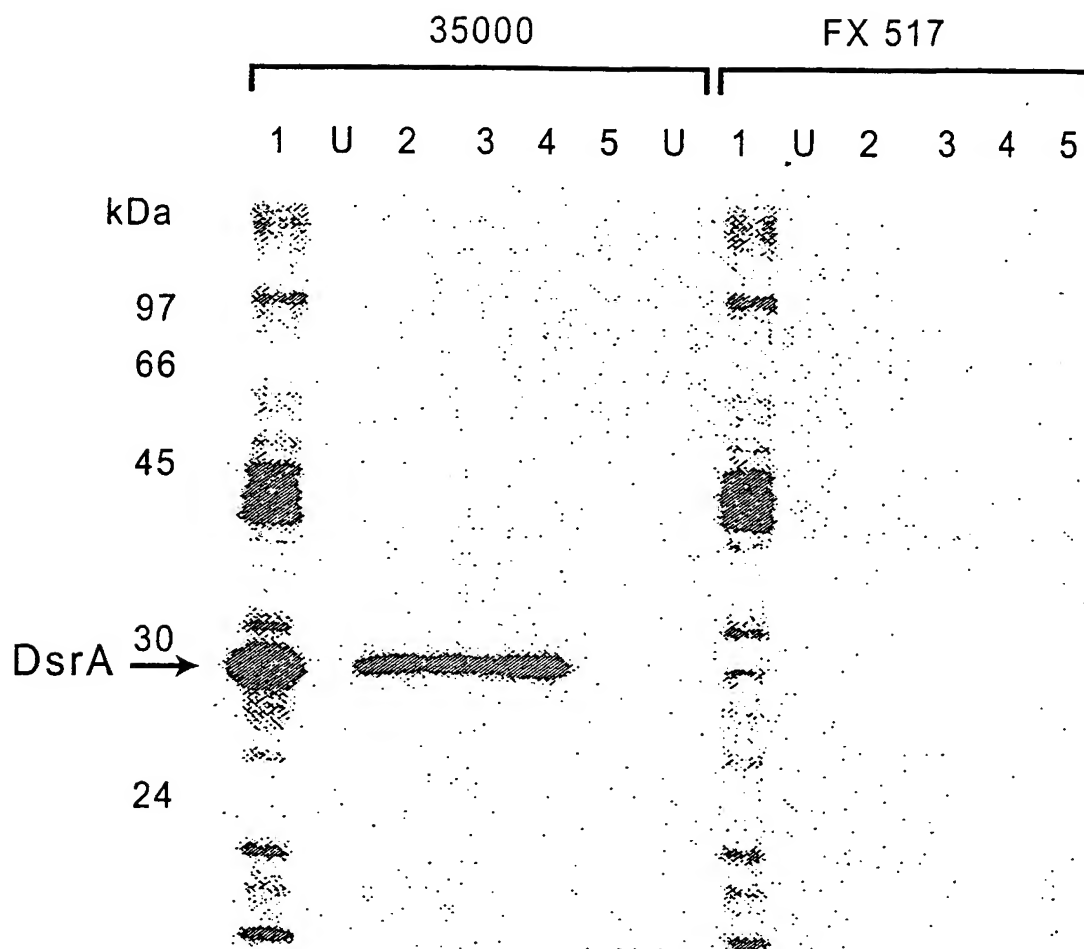


Fig. 12



U = Unlabeled OMP

1 = Surface-labeled *H. ducreyi* total protein

2 = Affinity purification, human native Vn

3 = Affinity purification, human recombinant Vn

4 = Affinity purification, bovine native Vn